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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=21; hr=13; min=42; sec=21; ms=289;]

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Application No: 10555289 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-07-01 15:59:51.257
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 124 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 32
Actual SeqID Count: 32

Error code	Error Description
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SEQUENCE LISTING

<110> BATTINI, JEAN-LUC GEORGES LAURENT
 MANEL, NICOLAS GABRIEL ALBERT
 KIM, FELIX JINHYUN
 KINET, SANDRINA
 TAYLOR, NAOMI
 SITBON, MARC

<120> GLUT-1 AS A RECEPTOR FOR HTLV ENVELOPES AND ITS USES

<130> 0508-1149

<140> 10555289

<141> 2008-07-01

<150> PCT/EP2004/004624

<151> 2004-04-30

<150> EP 03291067.1

<151> 2003-05-02

<160> 32

<170> PatentIn Ver. 3.3

<210> 1

<211> 1479

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1476)

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gga gga gca gtg ctt ggc tcc ctg cag ttt ggc tac aac act gga gtc	96
Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val	
20 25 30	

atc aat gcc ccc cag aag gtg atc gag gag ttc tac aac cag aca tgg	144
Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp	
35 40 45	

gtc cac cgc tat ggg gag agc atc ctg ccc acc acg ctc acc acg ctc	192
Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu	
50 55 60	

tgg tcc ctc tca gtg gcc atc ttt tct gtt ggg ggc atg att ggc tcc	240
Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser	
65 70 75 80	

ttc tct gtg ggc ctt ttc gtt aac cgc ttt ggc cgg cgg aat tca atg	288
Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met	
85 90 95	
ctg atg atg aac ctg ctg gcc ttc gtg tcc gcc gtg ctc atg ggc ttc	336
Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe	
100 105 110	
tcg aaa ctg ggc aag tcc ttt gag atg ctg atc ctg ggc cgc ttc atc	384
Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile	
115 120 125	
atc ggt gtg tac tgc ggc ctg acc aca ggc ttc gtg ccc atg tat gtg	432
Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val	
130 135 140	
ggt gaa gtg tca ccc aca gcc ttt cgt ggg gcc ctg ggc acc ctg cac	480
Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His	
145 150 155 160	
cag ctg ggc atc gtc gtc ggc atc ctc atc gcc cag gtg ttc ggc ctg	528
Gln Leu Gly Ile Val Val Gly Ile Leu Ile Ala Gln Val Phe Gly Leu	
165 170 175	
gac tcc atc atg ggc aac aag gac ctg tgg ccc ctg ctg ctg agc atc	576
Asp Ser Ile Met Gly Asn Lys Asp Leu Trp Pro Leu Leu Leu Ser Ile	
180 185 190	
atc ttc atc ccg gcc ctg ctg cag tgc atc gtg ctg ccc ttc tgc ccc	624
Ile Phe Ile Pro Ala Leu Leu Gln Cys Ile Val Leu Pro Phe Cys Pro	
195 200 205	
gag agt ccc cgc ttc ctg ctc atc aac cgc aac gag gag aac cgg gcc	672
Glu Ser Pro Arg Phe Leu Leu Ile Asn Arg Asn Glu Glu Asn Arg Ala	
210 215 220	
aag agt gtg cta aag aag ctg cgc ggg aca gct gac gtg acc cat gac	720
Lys Ser Val Leu Lys Lys Leu Arg Gly Thr Ala Asp Val Thr His Asp	
225 230 235 240	
ctg cag gag atg aag gaa gag agt cgg cag atg atg cgg gag aag aag	768
Leu Gln Glu Met Lys Glu Glu Ser Arg Gln Met Met Arg Glu Lys Lys	
245 250 255	
gtc acc atc ctg gag ctg ttc cgc tcc ccc gcc tac cgc cag ccc atc	816
Val Thr Ile Leu Glu Leu Phe Arg Ser Pro Ala Tyr Arg Gln Pro Ile	
260 265 270	
ctc atc gct gtg gtg ctg cag ctg tcc cag cag ctg tct ggc atc aac	864
Leu Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn	
275 280 285	
gct gtc ttc tat tac tcc acg agc atc ttc gag aag gcg ggg gtg cag	912
Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Lys Ala Gly Val Gln	
290 295 300	
cag cct gtg tat gcc acc att ggc tcc ggt atc gtc aac acg gcc ttc	960

Gln Pro Val Tyr Ala Thr Ile Gly Ser Gly Ile Val Asn Thr Ala Phe
 305 310 315 320

 act gtc gtg tcg ctg ttt gtg gtg gag cga gca ggc cgg cgg acc ctg 1008
 Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu
 325 330 335

 cac ctc ata ggc ctc gct ggc atg gcg ggt tgt gcc ata ctc atg acc 1056
 His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr
 340 345 350

 atc gcg cta gca ctg ctg gag cag cta ccc tgg atg tcc tat ctg agc 1104
 Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser
 355 360 365

 atc gtg gcc atc ttt ggc ttt gtg gcc ttc ttt gaa gtg ggt cct ggc 1152
 Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly
 370 375 380

 ccc atc cca tgg ttc atc gtg gct gaa ctc ttc agc cag ggt cca cgt 1200
 Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
 385 390 395 400

 cca gct gcc att gcc gtt gca ggc ttc tcc aac tgg acc tca aat ttc 1248
 Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
 405 410 415

 att gtg ggc atg tgc ttc cag tat gtg gag caa ctg tgt ggt ccc tac 1296
 Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
 420 425 430

 gtc ttc atc atc ttc act gtg ctc ctg gtt ctg ttc ttc atc ttc acc 1344
 Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
 435 440 445

 tac ttc aaa gtt cct gag act aaa ggc cgg acc ttc gat gag atc gct 1392
 Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
 450 455 460

 tcc ggc ttc cgg cag ggg gga gcc agc caa agt gat aag aca ccc gag 1440
 Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
 465 470 475 480

 gag ctg ttc cat ccc ctg ggg gct gat tcc caa gtg tga 1479
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 485 490

<210> 2

<211> 492

<212> PRT

<213> Homo sapiens

<400> 2

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Ile	Asn	Ala	Pro	Gln	Lys	Val	Ile	Glu	Glu	Phe	Tyr	Asn	Gln	Thr	Trp	35	40	45
Val	His	Arg	Tyr	Gly	Glu	Ser	Ile	Leu	Pro	Thr	Thr	Leu	Thr	Thr	Leu	50	55	60
Trp	Ser	Leu	Ser	Val	Ala	Ile	Phe	Ser	Val	Gly	Gly	Met	Ile	Gly	Ser	65	70	75
Phe	Ser	Val	Gly	Leu	Phe	Val	Asn	Arg	Phe	Gly	Arg	Arg	Asn	Ser	Met	85	90	95
Leu	Met	Met	Asn	Leu	Leu	Ala	Phe	Val	Ser	Ala	Val	Leu	Met	Gly	Phe	100	105	110
Ser	Lys	Leu	Gly	Lys	Ser	Phe	Glu	Met	Leu	Ile	Leu	Gly	Arg	Phe	Ile	115	120	125
Ile	Gly	Val	Tyr	Cys	Gly	Leu	Thr	Thr	Gly	Phe	Val	Pro	Met	Tyr	Val	130	135	140
Gly	Glu	Val	Ser	Pro	Thr	Ala	Phe	Arg	Gly	Ala	Leu	Gly	Thr	Leu	His	145	150	155
Gln	Leu	Gly	Ile	Val	Val	Gly	Ile	Leu	Ile	Ala	Gln	Val	Phe	Gly	Leu	165	170	175
Asp	Ser	Ile	Met	Gly	Asn	Lys	Asp	Leu	Trp	Pro	Leu	Leu	Leu	Ser	Ile	180	185	190
Ile	Phe	Ile	Pro	Ala	Leu	Leu	Gln	Cys	Ile	Val	Leu	Pro	Phe	Cys	Pro	195	200	205
Glu	Ser	Pro	Arg	Phe	Leu	Leu	Ile	Asn	Arg	Asn	Glu	Glu	Asn	Arg	Ala	210	215	220
Lys	Ser	Val	Leu	Lys	Lys	Leu	Arg	Gly	Thr	Ala	Asp	Val	Thr	His	Asp	225	230	235
Leu	Gln	Glu	Met	Lys	Glu	Glu	Ser	Arg	Gln	Met	Met	Arg	Glu	Lys	Lys	245	250	255
Val	Thr	Ile	Leu	Glu	Leu	Phe	Arg	Ser	Pro	Ala	Tyr	Arg	Gln	Pro	Ile	260	265	270
Leu	Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser	Gly	Ile	Asn	275	280	285
Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Lys	Ala	Gly	Val	Gln	290	295	300
Gln	Pro	Val	Tyr	Ala	Thr	Ile	Gly	Ser	Gly	Ile	Val	Asn	Thr	Ala	Phe	305	310	315
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Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu
 325 330 335
 His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr
 340 345 350
 Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser
 355 360 365
 Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly
 370 375 380
 Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
 385 390 395 400
 Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
 405 410 415
 Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
 420 425 430
 Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
 435 440 445
 Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
 450 455 460
 Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
 465 470 475 480
 Glu Leu Phe His Pro Leu Gly Ala Asp Ser Gln Val
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<210> 3

<211> 924

<212> DNA

<213> Human T-cell lymphotropic virus type 1

<220>

<221> CDS

<222> (1)..(924)

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 ctc atc ctc ggt gat tac agc ccc agc tgc tgt act ctc aca att gga 96
 Leu Ile Leu Gly Asp Tyr Ser Pro Ser Cys Cys Thr Leu Thr Ile Gly
 20 25 30
 gtc tcc tca tac cac tct aaa ccc tgc aat cct gcc cag cca gtt tgt 144
 Val Ser Ser Tyr His Ser Lys Pro Cys Asn Pro Ala Gln Pro Val Cys
 35 40 45
 tcg tgg acc ctc gac ctg ctg gcc ctt tca gcg gat cag gcc cta cag 192

Ser Trp Thr Leu Asp Leu Leu Ala Leu Ser Ala Asp Gln Ala Leu Gln	
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ccc ccc tgc cct aat cta gta agt tac tcc agc tac cat gcc acc tat	240
Pro Pro Cys Pro Asn Leu Val Ser Tyr Ser Ser Tyr His Ala Thr Tyr	
65 70 75 80	
tcc cta tat cta ttc cct cat tgg att aaa aag cca aac cga aat ggc	288
Ser Leu Tyr Leu Phe Pro His Trp Ile Lys Lys Pro Asn Arg Asn Gly	
85 90 95	
gga ggc tat tat tca gcc tct tat tca gac cct tgt tcc tta aag tgc	336
Gly Gly Tyr Tyr Ser Ala Ser Tyr Ser Asp Pro Cys Ser Leu Lys Cys	
100 105 110	
cca tac ctg ggg tgc caa tca tgg acc tgc ccc tat aca gga gcc gtc	384
Pro Tyr Leu Gly Cys Gln Ser Trp Thr Cys Pro Tyr Thr Gly Ala Val	
115 120 125	
tcc agc ccc tac tgg aag ttt cag caa gat gtc aat ttt act caa gaa	432
Ser Ser Pro Tyr Trp Lys Phe Gln Gln Asp Val Asn Phe Thr Gln Glu	
130 135 140	
gtt tca cgc ctc aat att aat ctc cat ttt tca aaa tgc ggt ttt ccc	480
Val Ser Arg Leu Asn Ile Asn Leu His Phe Ser Lys Cys Gly Phe Pro	
145 150 155 160	
ttc tcc ctt cta gtc gac gct cca gga tat gac ccc atc tgg ttc ctt	528
Phe Ser Leu Leu Val Asp Ala Pro Gly Tyr Asp Pro Ile Trp Phe Leu	
165 170 175	
aat acc gaa ccc agc caa ctg cct ccc acc gcc cct cct cta ctc ccc	576
Asn Thr Glu Pro Ser Gln Leu Pro Pro Thr Ala Pro Pro Leu Leu Pro	
180 185 190	
cac tct aac cta gac cac atc ctc gag ccc tct ata cca tgg aaa tca	624
His Ser Asn Leu Asp His Ile Leu Glu Pro Ser Ile Pro Trp Lys Ser	
195 200 205	
aaa ctc ctg acc ctt gtc cag tta acc cta caa agc act aat tat act	672
Lys Leu Leu Thr Leu Val Gln Leu Thr Leu Gln Ser Thr Asn Tyr Thr	
210 215 220	
tgc att gtc tgt atc gat cgt gcc agc cta tcc act tgg cac gtc cta	720
Cys Ile Val Cys Ile Asp Arg Ala Ser Leu Ser Thr Trp His Val Leu	
225 230 235 240	
tac tct ccc aac gtc tct gtt cca tcc tct tct tct acc ccc ctc ctt	768
Tyr Ser Pro Asn Val Ser Val Pro Ser Ser Ser Ser Thr Pro Leu Leu	
245 250 255	
tac cca tcg tta gcg ctt cca gcc ccc cac ctg acg tta cca ttt aac	816
Tyr Pro Ser Leu Ala Leu Pro Ala Pro His Leu Thr Leu Pro Phe Asn	
260 265 270	
tgg acc cac tgc ttt gac ccc cag att caa gct ata gtc tcc tcc ccc	864
Trp Thr His Cys Phe Asp Pro Gln Ile Gln Ala Ile Val Ser Ser Pro	

275

280

285

tgt cat aac tcc ctc atc ctg ccc ccc ttt tcc ttg tca cct gtt ccc 912
 Cys His Asn Ser Leu Ile Leu Pro Pro Phe Ser Leu Ser Pro Val Pro
 290 295 300

acc cta gga tcc 924
 Thr Leu Gly Ser
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<210> 4

<211> 308

<212> PRT

<213> Human T-cell lymphotropic virus type 1

<400> 4

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Val Ser Ser Tyr His Ser Lys Pro Cys Asn Pro Ala Gln Pro Val Cys
 35 40 45

Ser Trp Thr Leu Asp Leu Leu Ala Leu Ser Ala Asp Gln Ala Leu Gln
 50 55 60

Pro Pro Cys Pro Asn Leu Val Ser Tyr Ser Ser Tyr His Ala Thr Tyr
 65 70 75 80

Ser Leu Tyr Leu Phe Pro His Trp Ile Lys Lys Pro Asn Arg Asn Gly
 85 90 95

Gly Gly Tyr Tyr Ser Ala Ser Tyr Ser Asp Pro Cys Ser Leu Lys Cys
 100 105 110

Pro Tyr Leu Gly Cys Gln Ser Trp Thr Cys Pro Tyr Thr Gly Ala Val
 115 120 125

Ser Ser Pro Tyr Trp Lys Phe Gln Gln Asp Val Asn Phe Thr Gln Glu
 130 135 140

Val Ser Arg Leu Asn Ile Asn Leu His Phe Ser Lys Cys Gly Phe Pro
 145 150 155 160

Phe Ser Leu Leu Val Asp Ala Pro Gly Tyr Asp Pro Ile Trp Phe Leu
 165 170 175

Asn Thr Glu Pro Ser Gln Leu Pro Pro Thr Ala Pro Pro Leu Leu Pro
 180 185 190

His Ser Asn Leu Asp His Ile Leu Glu Pro Ser Ile Pro Trp Lys Ser
 195 200 205

Lys Leu Leu Thr Leu Val Gln Leu Thr Leu Gln Ser Thr Asn Tyr Thr

210

215

220

Cys Ile Val Cys Ile Asp Arg Ala Ser Leu Ser Thr Trp His Val Leu
225 230 235 240

Tyr Ser Pro Asn Val Ser Val Pro Ser Ser Ser Ser Thr Pro Leu Leu
245 250 255

Tyr Pro Ser Leu Ala Leu Pro Ala Pro His Leu Thr Leu Pro Phe Asn
260 265 270

Trp Thr His Cys Phe Asp Pro Gln Ile Gln Ala Ile Val Ser Ser Pro
275 280